Transcriptomics from Space: Linking Remote Sensing to Tree Gene Expression to Monitor Forest Responses to Water Availability

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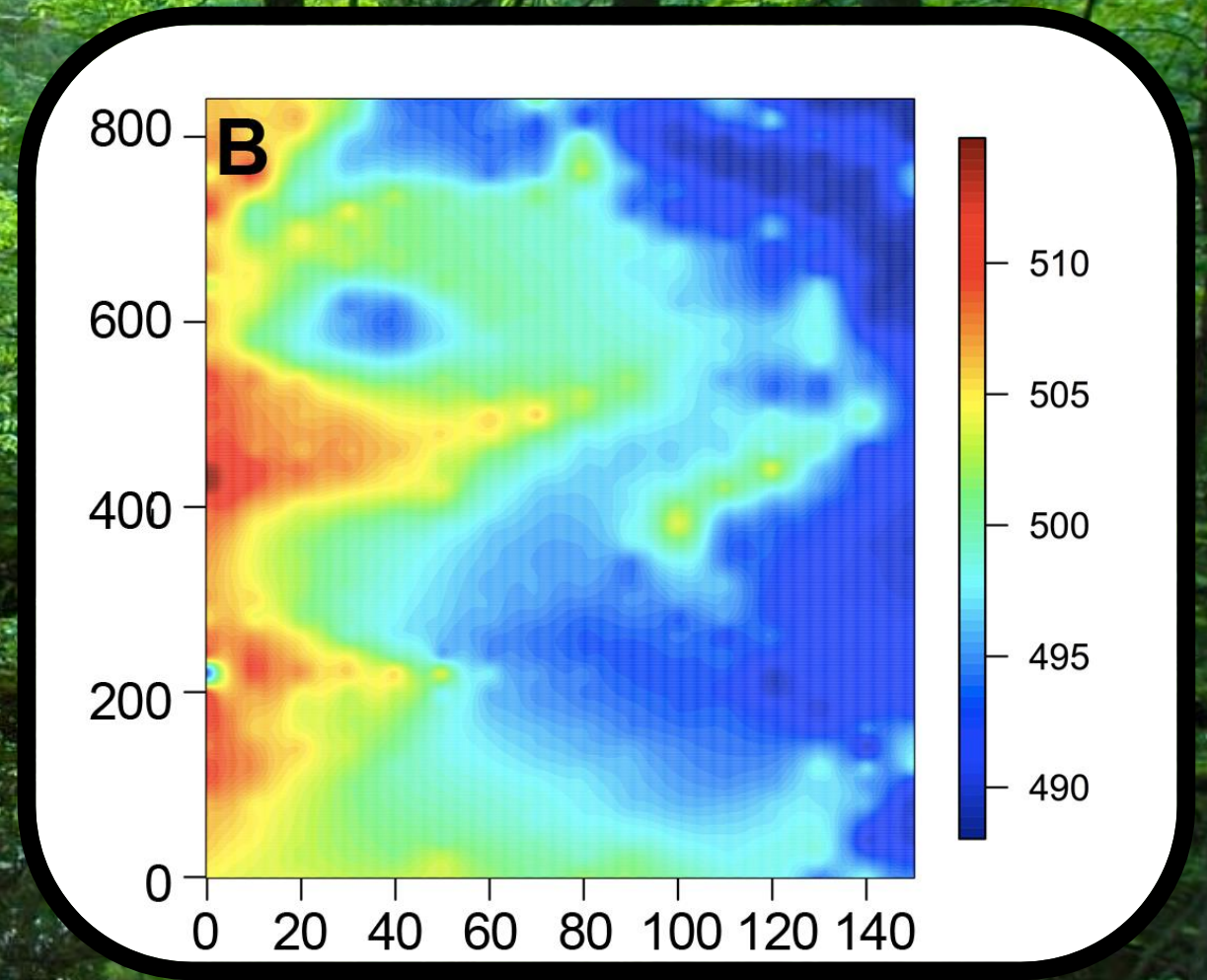www.swensonlab.com

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Community Transcriptomics In a Wisconsin Forest

Wabikon Forest Dynamics Plot, Nicolet NF, Wisconsin

Can we predict the spatial distributions of plants based upon differential gene expression in response to water availability?

What we have learned from community transcriptomics?

Dynamic functional responses to the environment are important

Transcriptomic data are typically superior predictors of tree distributions and growth as compared to functional trait data

Gene expression in the field is surprisingly predictable

Swenson et al. 2017. *Nat. Comm.*
Zambrano et al. 2017. *J. Ecol.*
Swenson et al. In Press. *Ecol. Lett.*
Sezen et al. In Review.

How do we estimate gene expression and how it changes through time at the scale of an entire national forest?

Can we build transcriptomically-informed systems to monitor forest health at these scales?

Can we predict gene expression from space?
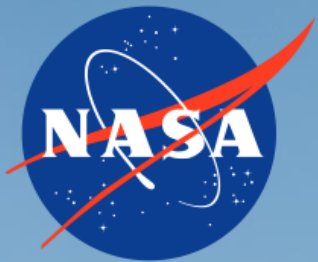
Objectives
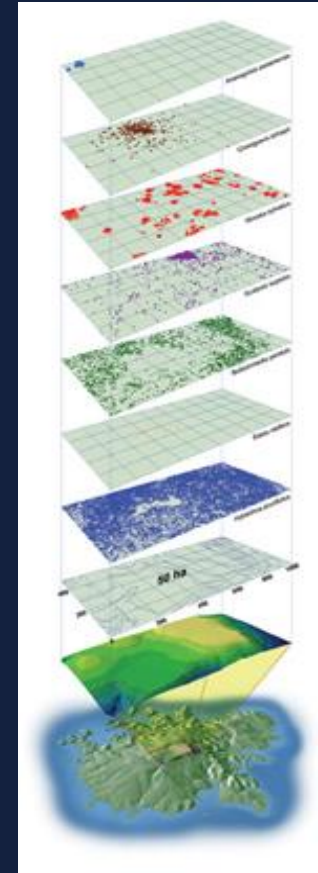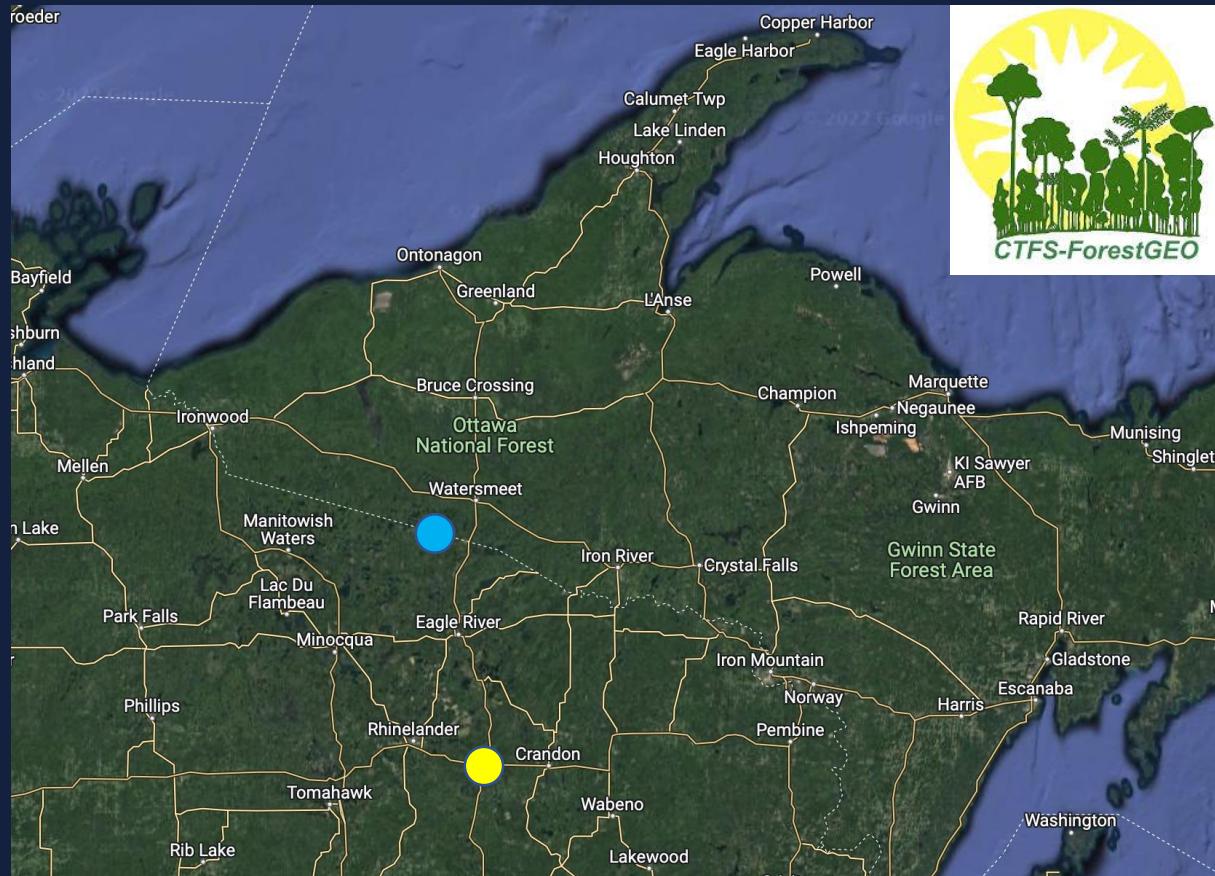
Establish the relationships between drought, spectral signatures and gene expression in the greenhouse

Study Sites

Study Sites – **Left)** The location of the Wabikon Lake (Yellow Dot) and UNDERC (Blue Dot) Forest Dynamics Plots. **Right)** A diagram of the data layers collected in a typical forest dynamics plot – topography and the distribution and diameter of every individual tree with a diameter 1cm or greater. Plots are re-censused every years in order to track changes in species distributions and diversity and individual growth and mortality.
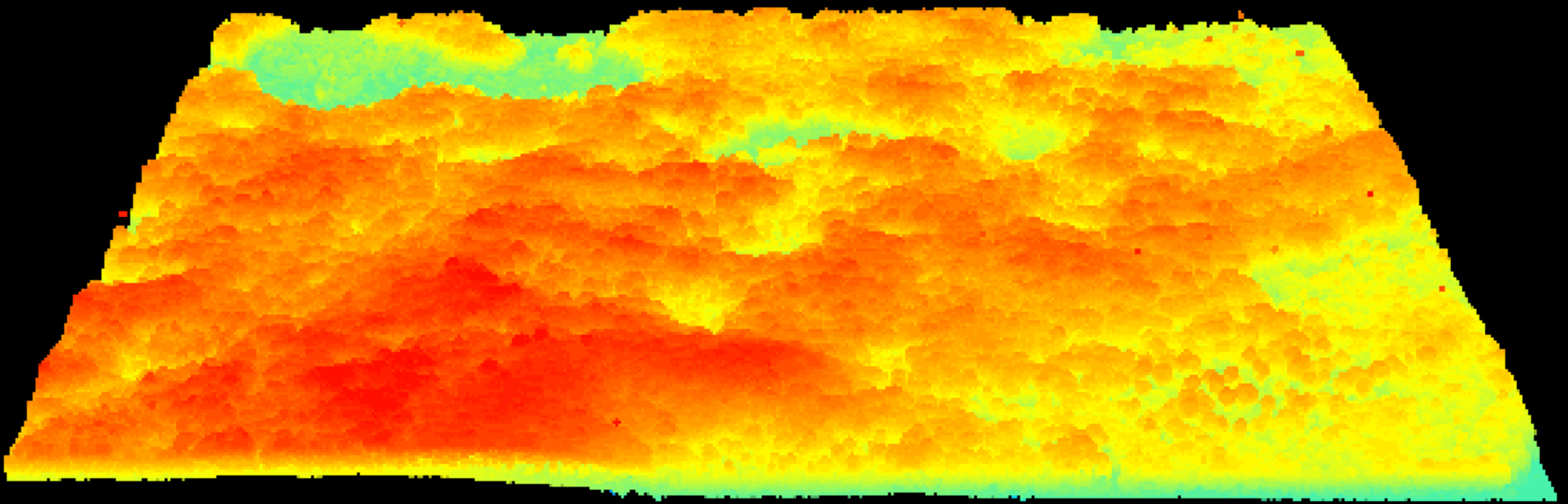
Objectives

Prediction of species composition and gene expression for sub-plots in the two forest dynamics plots throughout the growing season (i.e. as water stress increases from spring to late summer) using DESIS, GEDI and ECOSTRESS data products.
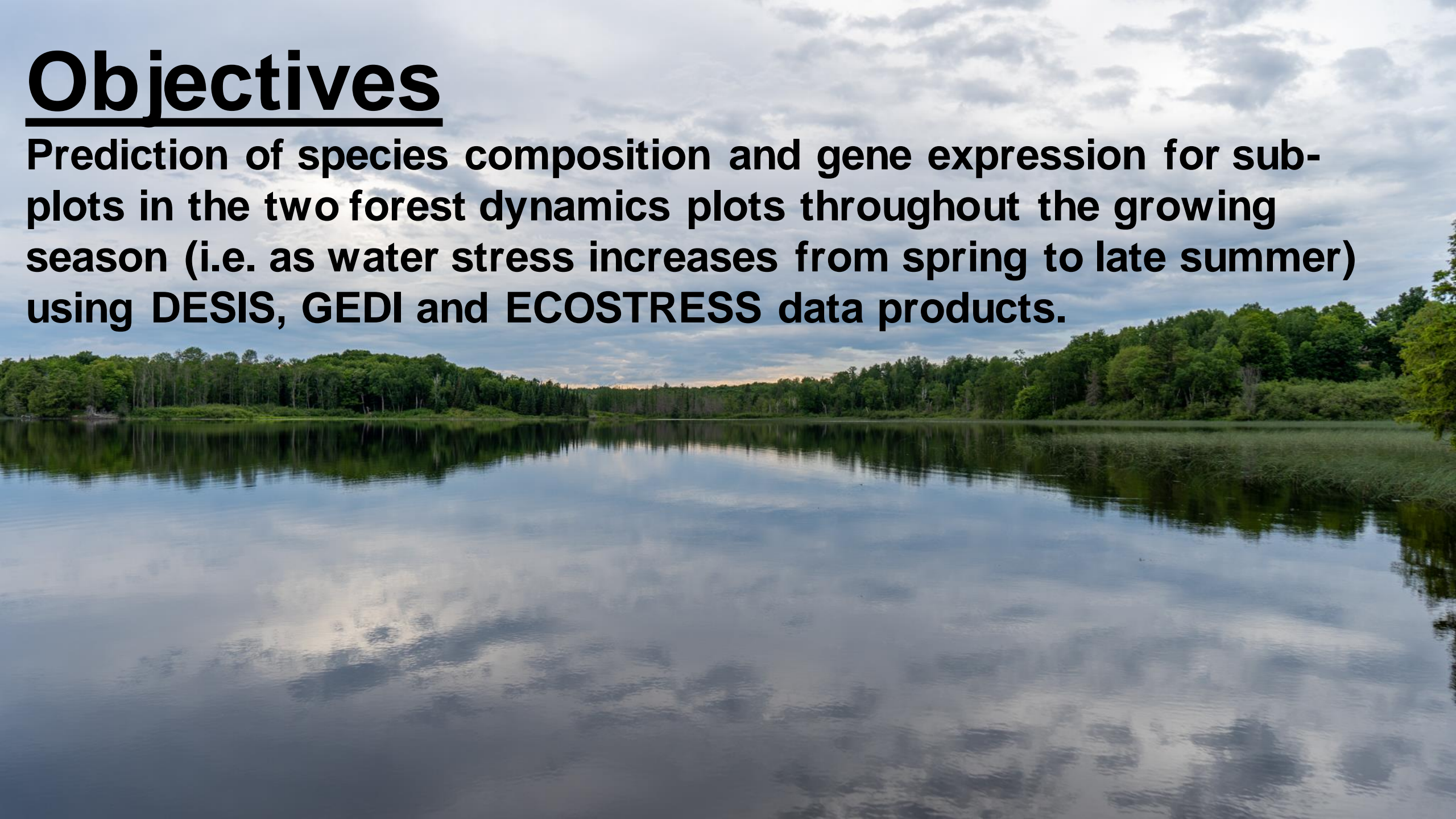
Objectives

Field validation of predictions by collecting spectral and gene expression data from individuals in the sub-plots throughout the growing season during two years.

Objectives

Build predictions of gene expression on the regional scale to serve as a system for identifying forested regions experiencing severe drought.

Acknowledgments

Collaborators
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